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| Terms | Documents |
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| L7 and PCR | 59 |

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| USPT,PGPB,JPAB,EPAB,DWPI,TDBD | L1 and tyrosine and substitut? | 66 | <u>L7</u> |
| USPT,PGPB,JPAB,EPAB,DWPI,TDBD | L1 and tyrosine | 326 | <u>L6</u> |
| USPT,PGPB,JPAB,EPAB,DWPI,TDBD | L1 and YxGG/A? | 0 | <u>L5</u> |
| USPT,PGPB,JPAB,EPAB,DWPI,TDBD | L1 and Y-GG/A? | 0 | <u>L4</u> |
| USPT,PGPB,JPAB,EPAB,DWPI,TDBD | L1 and Yx-gga? | 0 | <u>L3</u> |
| USPT,PGPB,JPAB,EPAB,DWPI,TDBD | L1 and GG/A? | 0 | <u>L2</u> |
| USPT,PGPB,JPAB,EPAB,DWPI,TDBD | DNA adj polymerase? | 1837 | <u>L1</u> |

**PALM INTRANET**

Day : Tuesday
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Time: 15:07:43

Inventor Name Search

Enter the **first few letters** of the Inventor's Last Name.
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NEWS 9 JUL 13 New SDI alert frequency now available in Derwent's
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NEWS 10 Aug 23 In-process records and more frequent updates now in
MEDLINE
NEWS 11 Aug 23 PAGE IMAGES FOR 1947-1966 RECORDS IN CAPLUS AND CA
NEWS 12 Aug 23 Adis Newsletters (ADISNEWS) now available on STN
NEWS 13 Sep 17 IMSworld Pharmaceutical Company Directory name change
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NEWS 14 Oct 09 Korean abstracts now included in Derwent World Patents
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NEWS 15 Oct 09 Number of Derwent World Patents Index updates increased
NEWS 16 Oct 15 Calculated properties now in the REGISTRY/ZREGISTRY File
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NEWS EXPRESS August 15 CURRENT WINDOWS VERSION IS V6.0c,
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| | ENTRY | SESSION |
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| FULL ESTIMATED COST | 0.15 | 0.15 |

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=> s DNA adj polymerase
L1 0 DNA ADJ POLYMERASE

=> s polymerase?
L2 712554 POLYMERASE?

=> s DNA?(a)polymerase
L3 91094 DNA?(A) POLYMERASE

=> s DNA?(a)polymerase?
L4 91103 DNA?(A) POLYMERASE?

=> s l4 and B?
TERM 'B?' EXCEEDED TRUNCATION LIMITS - SEARCH ENDED
1 FILES SEARCHED...

<-----User Break----->
u

SEARCH ENDED BY USER

You have entered a truncated stem which occurs in too many terms.
Make the stem longer and try again. For example, if your original
term was 'degr?' to search for variations and the abbreviation for
'degradation', you could replace it with the expression '(degrdn OR
degrad?)'. If your search term was numeric, e.g., 'C>5', reduce the
size of the range.

=> s l4 and (b-type)
L5 145 L4 AND (B-TYPE)

=> s l4 and B-type?
L6 145 L4 AND B-TYPE?

=> s l4 and B-?
ADDITIONAL CHARACTERS REQUIRED AFTER '?' FOR LEFT TRUNCATION
ADDITIONAL CHARACTERS REQUIRED AFTER '?' FOR LEFT TRUNCATION
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ADDITIONAL CHARACTERS REQUIRED AFTER '?' FOR LEFT TRUNCATION
ADDITIONAL CHARACTERS REQUIRED AFTER '?' FOR LEFT TRUNCATION
Additional characters must follow the left truncation symbol in your search term. If your search term contains a punctuation mark before the truncation symbol and you are searching in a field that uses implied proximity, the system may interpret the truncation symbol as being at the beginning of a term. Implied proximity is used in search fields indexed as single words, for example, the Basic Index. To see which fields in the current file have left truncation, enter "HELP SFIELDS" at an arrow prompt (=>).

```
=> s l6 and exonuclease?
L7          28 L6 AND EXONUCLEASE?
```

```
=> s l6 and polymerase?
L8          145 L6 AND POLYMERASE?
```

```
=> s l6 and Y-GG?A?
'?' TRUNCATION SYMBOL NOT VALID WITHIN 'GG?A?'
'?' TRUNCATION SYMBOL NOT VALID WITHIN 'GG?A?'
'?' TRUNCATION SYMBOL NOT VALID WITHIN 'GG?A?'
'?' TRUNCATION SYMBOL NOT VALID WITHIN 'GG?A?'
'?' TRUNCATION SYMBOL NOT VALID WITHIN 'GG?A?'
'?' TRUNCATION SYMBOL NOT VALID WITHIN 'GG?A?'
The truncation symbol ? may be used only at the end of a search
term. To specify a variable character within a word use '!', e.g.,
'wom!n' to search for both 'woman' and 'women'. Enter "HELP
TRUNCATION" at an arrow prompt (=>) for more information.
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=> s l6 and Y-GG/A?
'A?' IS NOT A VALID FIELD CODE
'A?' IS NOT A VALID FIELD CODE
'A?' IS NOT A VALID FIELD CODE
'A?' IS NOT A VALID FIELD CODE
'A?' IS NOT A VALID FIELD CODE
'A?' IS NOT A VALID FIELD CODE
L9          0 L6 AND Y-GG/A?
```

```
=> s l6 and gga?
L10         0 L6 AND GGA?
```

```
=> s l6 and y?
  4 FILES SEARCHED...
<-----User Break----->
u
SEARCH ENDED BY USER
```

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=> d history
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FILE 'MEDLINE, EMBASE, CAPLUS, SCISEARCH, BIOSIS, REGISTRY' ENTERED AT 13:01:33 ON 23 OCT 2001

```
L1          0 S DNA ADJ POLYMERASE
L2          712554 S POLYMERASE?
L3          91094 S DNA?(A) POLYMERASE
L4          91103 S DNA?(A) POLYMERASE?
L5          145 S L4 AND (B-TYPE)
L6          145 S L4 AND B-TYPE?
```

L7 28 S L6 AND EXONUCLEASE?
L8 145 S L6 AND POLYMERASE?
L9 0 S L6 AND Y-GG/A?
L10 0 S L6 AND GGA?

=> dup rem 17

DUPLICATE IS NOT AVAILABLE IN 'REGISTRY'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L7
COMMAND INTERRUPTED

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=> dup rem 17

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Desk by telephone or via SEND in the STNMAIL file.

=> s 17 and PCR

L13 7 L7 AND PCR

=> dup rem 113

DUPLICATE IS NOT AVAILABLE IN 'REGISTRY'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L13

L14 4 DUP REM L13 (3 DUPLICATES REMOVED)

=> d 114 ibib abs 1-

YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):y

L14 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2001:676310 CAPLUS

DOCUMENT NUMBER: 135:237584

TITLE: Methods of making mutant **B-type**
DNA polymerases from *Thermococcus*
aggregans with improved performance in **PCR**
INVENTOR(S): Sobek, Harald; Frey, Bruno; Antranikian, Garabed;
Boehlke, Kristina; Pisani, Francesca Maria; Rossi,
Mose

PATENT ASSIGNEE(S): Roche Diagnostics G.m.b.H., Germany

SOURCE: Eur. Pat. Appl., 40 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|--|------|----------|-----------------|----------|
| EP 1132474 | A1 | 20010912 | EP 2001-1104583 | 20010306 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | | |
| JP 2001269188 | A2 | 20011002 | JP 2001-61781 | 20010306 |
| PRIORITY APPLN. INFO.: EP 2000-105155 A 20000311 | | | | |
| AB The invention provides methods of making mutant B-type | | | | |

DNA polymerase with high performance in **PCR**.
In particular, the invention discloses that wild type **B-type DNA polymerases** have a Y-GG/A amino acid motif between the N-terminal 3'-5'-**exonuclease** domain and the C-terminal polymerase domain whereas the tyrosine of the Y-GG/A amino acid

motif is mutated and the mutant **DNA polymerases** are suitable for **PCR** and other nucleic acid synthesizing reactions, and have a better performance. The invention also provides methods of producing the mutants, vectors and cell lines comprising genes encoding the mutants.

REFERENCE COUNT: 4
REFERENCE(S): (1) Bohlke, K; NUCLEIC ACIDS RESEARCH 2000, V28(20), P3910 MEDLINE
(2) Boehringer Mannheim GmbH; DE 19611759 A 1997 CAPLUS
(3) Pisani, F; BIOCHEMISTRY 1998, V37(42), P15005 CAPLUS
(4) Truniger, V; EMBO JOURNAL 1996, V15(13), P3430 CAPLUS

L14 ANSWER 2 OF 4 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2000478261 MEDLINE
DOCUMENT NUMBER: 20482208 PubMed ID: 11024170
TITLE: **PCR performance of the B-type DNA polymerase** from the thermophilic euryarchaeon *Thermococcus aggregans* improved by mutations in the Y-GG/A motif.
AUTHOR: Bohlke K; Pisani F M; Vorgias C E; Frey B; Sobek H; Rossi M; Antranikian G
CORPORATE SOURCE: Institute of Technical Microbiology, Technical University Hamburg-Harburg, Denickestrabetae 15, 21073 Hamburg, Germany.
SOURCE: NUCLEIC ACIDS RESEARCH, (2000 Oct 15) 28 (20) 3910-7. Journal code: O8L; 0411011. ISSN: 1362-4962.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010521
Entered Medline: 20001031

AB The effect of mutations in the highly conserved Y-GG/A motif of **B-type DNA polymerases** was studied in the **DNA polymerase** from the hyperthermophilic euryarchaeon *Thermococcus aggregans*. This motif plays a critical role in the balance between the synthesis and degradation of the DNA chain. Five different mutations of the tyrosine at position 387 (Tyr387-->Phe, Tyr387-->Trp, Tyr387-->His, Tyr387-->Asn and Tyr387-->Ser) revealed that an aromatic ring system is crucial for the synthetic activity of the enzyme. Amino acids at this position lacking the ring system (Ser and Asn) led to a significant decrease in polymerase activity and to enhanced **exonuclease** activity, which resulted in improved enzyme fidelity. Exchange of tyrosine to phenylalanine, tryptophan or histidine led to phenotypes with wild-type-like fidelity but enhanced **PCR** performance that could be related to a higher velocity of polymerisation. With the help of a modelled structure of *T. aggregans* **DNA polymerase**, the biochemical data were interpreted proposing that the conformation of the flexible loop containing the Y-GG/A motif is an

important factor for the equilibrium between DNA polymerisation and exonucleolysis.

L14 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2001 ACS DUPLICATE 2
ACCESSION NUMBER: 2000:762603 CAPLUS
DOCUMENT NUMBER: 134:322588
TITLE: **PCR performance of the B-type DNA polymerase** from the thermophilic euryarchaeon *Thermococcus aggregans* improved by mutations in the Y-GG/A motif
AUTHOR(S): Bohike, Kristina; Pisani, Francesca M.; Vorgias, Constantinos E.; Frey, Bruno; Sobek, Harald; Rossi, Mose; Antranikian, Garabed
CORPORATE SOURCE: Institute of Technical Microbiology, Technical University Hamburg-Harburg, Hamburg, 21073, Germany
SOURCE: Nucleic Acids Res. (2000), 28(20), 3910-3917
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The effect of mutations in the highly conserved Y-GG/A motif of **B-type DNA polymerases** was studied in the **DNA polymerase** from the hyperthermophilic euryarchaeon *Thermococcus aggregans*. This motif plays a crit. role in the balance between the synthesis and degrdn. of the DNA chain. Five different mutations of the tyrosine at position 387 (Tyr387.fwdarw.Phe, Tyr387.fwdarw.Trp, Tyr387.fwdarw.His, Tyr387.fwdarw.Asn and Tyr387.fwdarw.Ser) revealed that an arom. ring system is crucial for the synthetic activity of the enzyme. Amino acids at this position lacking the ring system (Ser and Asn) led to a significant decrease in polymerase activity and to enhanced **exonuclease** activity, which resulted in improved enzyme fidelity. Exchange of tyrosine to phenylalanine, tryptophan or histidine led to phenotypes with wild-type-like fidelity but enhanced **PCR** performance that could be related to a higher velocity of polymn. With the help of a modeled structure of *T. aggregans* **DNA polymerase**, the biochem. data were interpreted proposing that the conformation of the flexible loop contg. the Y-GG/A motif is an important factor for the equil. between DNA polymn. and exonucleolysis.

REFERENCE COUNT: 37
REFERENCE(S): (1) Barnes, W; Proc Natl Acad Sci 1994, V91, P2216 CAPLUS
(2) Bult, C; Science 1996, V273, P1058 CAPLUS
(4) Cann, I; J Bacteriol 1999, V181, P5984 CAPLUS
(5) Cann, I; Proc Natl Acad Sci 1998, V95, P14250 CAPLUS
(6) Dong, Q; J Biol Chem 1993, V268, P24163 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:354514 CAPLUS
DOCUMENT NUMBER: 131:154392
TITLE: Molecular cloning, sequence and expression of Aa-polB, a mitochondrial gene encoding a family B **DNA polymerase** from the edible basidiomycete *Agrocybe aegerita*
AUTHOR(S): Bois, F.; Barroso, G.; Gonzalez, P.; Labarere, J.
CORPORATE SOURCE: Laboratoire de Genetique Moleculaire et d'Amelioration

des Champignons Cultives, CRA de Bordeaux, Villenave
d'Ornon Cedex, F-33883, Fr.

SOURCE: Mol. Gen. Genet. (1999), 261(3), 508-513
CODEN: MGGEAE; ISSN: 0026-8925

PUBLISHER: Springer-Verlag

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An ORF of 1716 nucleotides, putatively encoding a **DNA polymerase**, was characterized in the mitochondrial genome of the edible basidiomycete *Agrocybe aegerita*. The complete gene, named Aa-polB, and its flanking regions were cloned and sequenced from three overlapping restriction fragments. Aa-polB is located between the SSU rDNA (5' region) and a gene for tRNA Asn (3' region), and is sep. from these genes by two A +T-rich intergenic regions of 1048 (5' region) and 3864 (3' region) nucleotides, which lack repeated sequences of mitochondrial or plasmid origin. The deduced Aa-POLB protein shows extensive sequence similarity with the family B **DNA polymerases** encoded by genomes that rely on protein-primed replication (invertrons). The domains involved in the 3'.fwdarw.5' **exonuclease** (Exo I to III) and polymerase (Pol I to Pol V) activities were localized on the basis of conserved sequence motifs. The alignment of the Aa-POLB protein (571 amino acids) with sequences of family B **DNA polymerases** from invertrons revealed that in Aa-POLB the N-terminal region preceding Exo I is short, suggesting a close relationship with the **DNA polymerases** of bacteriophages that have linear DNA. The Aa-polB gene was shown to be present in all wild strains examd., which were collected from a wide range of locations in Europe. As shown by RT-PCR, the Aa-polB gene is transcribed in the mitochondria, at a low but significant level. The likelihood of the coexistence of Aa-POLB and Pol .gamma. in the *A. aegerita* mitochondrion is discussed in the light of recent reports showing the conservation of the nucleus-encoded Pol .gamma. from yeast to human.

REFERENCE COUNT: 28

REFERENCE(S): (1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(2) Barroso, G; Appl Environ Microbiol 1995, V61, P1187 CAPLUS
(3) Blanco, L; Gene 1991, V100, P27 CAPLUS
(6) Coleman, A; J Protozool 1991, V38, P129 CAPLUS
(7) Dohmen, G; Curr Genet 1994, V25, P59 CAPLUS

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